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## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/767,561

Source: IFW&O

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## **RAW SEQUENCE LISTING**

DATE: 03/07/2005

PATENT APPLICATION: US/10/767,561

TIME: 15:24:12

Input Set : N:\Crf4\Refhold\10\_folder\J767561.raw

Output Set: N:\CRF4\03072005\J767561.raw

## **SEQUENCE LISTING**

1 (1) GENERAL INFORMATION:  
2     (i) APPLICANT: Freeman, Gordon J.  
3                         Nadler, Lee M.  
4                         Gray, Gary S.  
5     (ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3  
6                         WITH INCREASED IMMUNOGENICITY AND USES THEREFOR  
7     (iii) NUMBER OF SEQUENCES: 8  
8     (iv) CORRESPONDENCE ADDRESS:  
9         (A) ADDRESSEE: LAHIVE & COCKFIELD  
0         (B) STREET: 60 State Street, Suite 510  
1         (C) CITY: Boston  
2         (D) STATE: Massachusetts  
3         (E) COUNTRY: USA  
4         (F) ZIP: 02109  
5     (v) COMPUTER READABLE FORM:  
6         (A) MEDIUM TYPE: Floppy disk  
7         (B) COMPUTER: IBM PC compatible  
8         (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
9         (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
0     (vi) CURRENT APPLICATION DATA:  
1         (A) APPLICATION NUMBER: US/10/767,561  
2         (B) FILING DATE: 28-Jan-2004  
3         (C) CLASSIFICATION:  
4     (vii) PRIOR APPLICATION DATA:  
5         (A) APPLICATION NUMBER: US/09/206,132  
6         (B) FILING DATE: 07-DEC-1998  
7         (A) APPLICATION NUMBER: 08/456,104  
8         (B) FILING DATE:  
9         (A) APPLICATION NUMBER: 08/101,624  
0         (B) FILING DATE: 26-JUL-1993  
1         (A) APPLICATION NUMBER: 08/109,393  
2         (B) FILING DATE: 19-AUG-1993  
3     (viii) ATTORNEY/AGENT INFORMATION:  
4         (A) NAME: Mandragouras, Amy E.  
5         (B) REGISTRATION NUMBER: 36,207  
6         (C) REFERENCE/DOCKET NUMBER: RPI-008  
7     (ix) TELECOMMUNICATION INFORMATION:  
8         (A) TELEPHONE: (617) 227-7400  
9         (B) TELEFAX: (617) 227-5941  
0 (2) INFORMATION FOR SEQ ID NO: 1:  
1     (i) SEQUENCE CHARACTERISTICS:  
2         (A) LENGTH: 1120 base pairs

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43	(B) TYPE: nucleic acid	
44	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
46	(ii) MOLECULE TYPE: cDNA	
47	(ix) FEATURE:	
48	(A) NAME/KEY: CDS	
49	(B) LOCATION: 107..1093	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
51	CACAGGGTGA AAGCTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
52	GAGTGGGGTC ATTTCCAGAT ATTAGGTAC AGCAGAAAGCA GCCAAA ATG GAT CCC	115
53	Met Asp Pro	
54	1	
55	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
56	Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
57	5 10 15	
58	CTC TCT GGT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
59	Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
60	20 25 30 35	
61	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
62	Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
63	40 45 50	
64	GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
65	Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
66	55 60 65	
67	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
68	Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
69	70 75 80	
70	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
71	Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
72	85 90 95	
73	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
74	Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
75	100 105 110 115	
76	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
77	Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
78	120 125 130	
79	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
80	Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
81	135 140 145	
82	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
83	Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
84	150 155 160	
85	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
86	Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
87	165 170 175	
88	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
89	Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
90	180 185 190 195	
91	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739

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92	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr
93				200				205								210
94	AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT
95	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu
96			215					220								225
97	TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA
98	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro
99			230				235									240
100	GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT
101	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys
102		245				250										255
103	GTG	ATG	GTT	TTC	TGT	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG
104	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg
105	260				265				270							275
106	CCT	CGC	AAC	TCT	TAT	AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG
107	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu
108			280				285									290
109	AGT	GAA	CAG	ACC	AAG	AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT
110	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser
111		295				300										305
112	GAT	GAA	GCC	CAG	CGT	GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC
113	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp
114		310				315										320
115	AAA	AGT	GAT	ACA	TGT	TTT	TAATTAAAGA	GTAAAGCCCA	AAAAAAA							1120
116	Lys	Ser	Asp	Thr	Cys	Phe										
117		325														
119	(2)	INFORMATION FOR SEQ ID NO: 2:														
120	(i)	SEQUENCE CHARACTERISTICS:														
121	(A)	LENGTH: 329 amino acids														
122	(B)	TYPE: amino acid														
123	(D)	TOPOLOGY: linear														
124	(ii)	MOLECULE TYPE: protein														
125	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:														
126	Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met
127	1				5				10							15
128	Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe
129		20				25										30
130	Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln
131		35				40										45
132	Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val
133		50				55										60
134	Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser
135		65				70										80
136	Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg
137			85				90									95
138	Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile
139			100				105									110
140	His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser
141			115				120									125

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142 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile  
 143 130 135 140  
 144 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile  
 145 145 150 155 160  
 146 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys  
 147 165 170 175  
 148 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn  
 149 180 185 190  
 150 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro  
 151 195 200 205  
 152 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys  
 153 210 215 220  
 154 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln  
 155 225 230 235 240  
 156 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val  
 157 245 250 255  
 158 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys  
 159 260 265 270  
 160 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu  
 161 275 280 285  
 162 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro  
 163 290 295 300  
 164 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser  
 165 305 310 315 320  
 166 Ser Cys Asp Lys Ser Asp Thr Cys Phe  
 167 325  
 168 (2) INFORMATION FOR SEQ ID NO: 3:  
 169 (i) SEQUENCE CHARACTERISTICS:  
 170 (A) LENGTH: 1151 base pairs  
 171 (B) TYPE: nucleic acid  
 172 (C) STRANDEDNESS: double  
 173 (D) TOPOLOGY: linear  
 174 (ii) MOLECULE TYPE: cDNA  
 175 (ix) FEATURE:  
 176 (A) NAME/KEY: CDS  
 177 (B) LOCATION: 99..1028  
 178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 179 GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT  
 180 CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC 60  
 181 Met Asp  
 182 1  
 183 1  
 184 CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG  
 185 Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu  
 186 5 10 15  
 187 CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG  
 188 Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly  
 189 20 25 30  
 190 ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG  
 191 Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu

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192	35	40	45	50	
193	AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC				296
194	Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr				
195	55	60	65		
196	GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC				344
197	Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr				
198	70	75	80		
199	CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC				392
200	Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His				
201	85	90	95		
202	AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA				440
203	Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys				
204	100	105	110		
205	AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG				488
206	Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu				
207	115	120	125	130	
208	TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT				536
209	Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn				
210	135	140	145		
211	GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT				584
212	Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly				
213	150	155	160		
214	CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT				632
215	His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn				
216	165	170	175		
217	GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG				680
218	Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu				
219	180	185	190		
220	TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG				728
221	Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp				
222	195	200	205	210	
223	CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC				776
224	His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser				
225	215	220	225		
226	TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT				824
227	Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr				
228	230	235	240		
229	TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG				872
230	Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Val Met				
231	245	250	255		
232	CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC				920
233	Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro				
234	260	265	270		
235	AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG				968
236	Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu				
237	275	280	285	290	
238	ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA				1016
239	Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro				
240	295	300	305		

**VERIFICATION SUMMARY**

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Input Set : N:\Crf4\Refhold\10\_folder\J767561.raw

Output Set: N:\CRF4\03072005\J767561.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)  
L:441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7